

OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids I; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	DR	PROSITE; PS00305; 11S SEED STORAGE; 1.
OC	NCBI_TAXID=1848;	KW	Seed storage protein; Storage protein.
OX		SEQUENCE	517 AA; 58229 MW; 0E1591BC72181B7C CRC64;
RN		Query Match	100.0%; Score 58; DB 2; Length 517;
[1]	SEQUENCE FROM N.A.	Best Local Similarity	100.0%; Pred. No. 0.71; Mismatches 0; Indels 0; Gaps 0;
RX	MEDLINE=95241635; PubMed=7724684;	Matches	
RX	Wang W.M., Gao X.S.; Zhuang N.J.; Xu M.L.; Xue Z.T.; et	Qy	1 IPPGVYWT 9
RX	RT		
RX	RTCC. "The Glycinin A384 mRNA from wild soybean Glycine soja Sieb. et	Db	149 IPPGVYWT 157
CC	-I- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).		
CC	-I- SIMILARITY: Belongs to the 11S seed storage protein (globulins) family.	RESULT 4	
CC	EMBL; X79467; CAA55977.1; -.	Q9SSD0	PRELIMINARY; PRT; 560 AA.
DR	PR00806; PQ00806.	ID	Q9SSD0
DR	PIR; PQ00807; PQ00807.	AC	Q9SSD0; Created
DR	PIR; PQ00808; PQ00808.	DT	01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DR	HSSP; P04776; 1FZ2.	DT	01-MAY-2000 (TREMBLrel. 13; Last annotation update)
DR	GO; GO:0045725; F: nutrient reservoir activity; IEA.	DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)
DR	InterPro; IPR006045; Cupin.	DE	Glycinin G4 subunit.
DR	InterPro; IPR007113; Cupin region.	OS	Glycine max (Soybean).
DR	InterPro; IPR011051; RmLC-like cupin.	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
PFam	PF00190; Cupin; 2.	OC	eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
DR	PRINTS; PR00439; 11SGLOBULIN.	NCBI_TaxID=3847;	NCBI_TaxID=3847;
DR	PROSITE; PS00305; 11S_SEED_STORAGE; 1.	RN	[1]
KW	Seed storage protein; Storage protein.	RP	SEQUENCE FROM N.A. PubMed=2485233;
SEQUENCE	517 AA; 58187 MW; 0440FF44C72181B7C CRC64;	RX	RXN
Query Match	100.0%; Score 58; DB 2; Length 517;	RA	NIelsen N.C.; Dickinson C.D.; Cho T.J.; Thanh V.H.; Scallon B.J.,
Best Local Similarity	100.0%; Pred. No. 0.71; 0; Indels 0; Gaps 0;	RA	Fischer R.L.; Sims T.L.; Drews G.N.; Goldberg R.B.;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RT	"Characterization of the Glycinin gene family in soybean.";
Qy	1 IPPGVYWT 9	RL	Plant Cell 1:313-328 (1989).
Db	149 IPPGVYWT 157	CC	-I- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).
CC	-I- SIMILARITY: Belongs to the 11S seed storage protein (globulins) family.	CC	-I- SIMILARITY: Belongs to the 11S seed storage protein (globulins) family.
DR	PIR; S11004; S11004.	CC	-I- SIMILARITY: Belongs to the 11S seed storage protein (globulins) family.
DR	HSSP; P04776; 1FZ2.	DR	DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR	GO; GO:0045735; F: nutrient reservoir activity; IEA.	DR	DR InterPro; IPR006045; Cupin.
DR	InterPro; IPR011051; RmLC-like cupin.	DR	DR InterPro; IPR011051; RmLC-like cupin.
DR	InterPro; IPR006044; Seedstore_11s.	DR	DR InterPro; IPR006044; Seedstore_11s.
PFam	PF00190; Cupin; 2.	DR	DR PRINTS; PR00439; 11SGLOBULIN.
DR	PRINTS; PR00439; 11SGLOBULIN.	DR	DR PROSITE; PS00305; 11S_SEED_STORAGE; 1.
DR	GO; GO:0045735; F: nutrient reservoir activity; IEA.	SQ	DR SEQUENCE 560 AA; 65679 MW; F95DBEA4012DDA024 CRC64;
DR	InterPro; IPR006044; Seedstore_11s.	Qy	Query Match 100.0%; Score 58; DB 2; Length 560;
DR	InterPro; IPR006044; Seedstore_11s.	DR	Best Local Similarity 100.0%; Pred. No. 0.77; Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR006044; Seedstore_11s.	Db	1 IPPGVYWT 9
DR	InterPro; IPR006044; Seedstore_11s.	DR	149 IPPGVYWT 157
DR	InterPro; IPR006044; Seedstore_11s.	RESULT 5	
DR	InterPro; IPR006044; Seedstore_11s.	Q43452	PRELIMINARY; PRT; 562 AA.
DR	InterPro; IPR006044; Seedstore_11s.	ID	Q43452; Created
DR	InterPro; IPR006045; Cupin.	AC	Q43452; Last sequence update)
DR	InterPro; IPR007113; Cupin region.	DT	01-NOV-1996 (TREMBLrel. 01; Last sequence update)
DR	InterPro; IPR01051; RmLC-like cupin.	DT	01-NOV-1996 (TREMBLrel. 01; Last sequence update)
DR	InterPro; IPR006044; Seedstore_11s.	DE	Glycinin max (Soybean).
DR	InterPro; IPR006044; Seedstore_11s.	OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
PFam	PFam; PR00190; Cupin; 2.	OC	eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
DR	PFam; PR00190; Cupin; 2.	NC	NCBI_TaxID=3847;
DR	PRINTS; PR00439; 11SGLOBULIN.	RN	[1]

SEQUENCE FROM N.A.
 TISSUE=leaf;
 MEDLINE=922056911; PubMed=11316192;
 Xue Z.T.; Xu M.L.; Shen W.; Zhuang N.L.; Hu W.M.; Shen S.C.;
 "Characterization of the Gy4 Glycine gene from soybean Glycine max cv.
 Forrest";
 Plant Mol. Biol. 18:897-908(1992).
 [2]

SEQUENCE FROM N.A.
 TISSUE=leaf;
 RA Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.
 -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 basic chain derived from a single precursor and linked by a
 disulfide bond (By similarity).
 CC -1- SIMILARITY: Belongs to the IIS seed storage protein (globulins)
 family.
 EMBL; X52863; CAA37044.1; -.
 DR PIR; PQ0159; PQ0199.
 PIR; S20946; S20946.
 DR HSSP; PQ4776; 1FXZ.
 DR GO; GO:0045735; P:nutrient reservoir activity; IEA.
 DR InterPro; IPR00645; Cupin.
 DR InterPro; IPR011051; RmLC.
 DR InterPro; IPR006044; Seedstore_11s.
 PFAM; PF00190; Cupin; 2.
 DR PROSITE; PRO0439; 11SG1G0BULIN.
 DR PROSITE; PS00305; IIS_SEED_STORAGE; 1.
 KW SIGNAL.
 FT CHAIN 1 23 Potential.
 FT CHAIN 24 562 Glycinin.
 SEQUENCE 562 AA; 63876 MW; 3A4EF285448AB15A CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 562;
 Best Local Similarity 100.0%; Pred. No. 0.77;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IPPGYPYWT 9
 Db 148 IPPGYPYWT 156

RESULT 6
 Q39921; PRELIMINARY; PRT; 563 AA.
 AC Q39921;
 DT 01-NOV-1996 (TRIMBULrel. 01, Created)
 DT 01-NOV-1996 (TRIMBULrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRIMBULrel. 24, Last annotation update)
 GN Name=Glycinin Gy4;
 OS Glycine soja (wild soybean).
 OC Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
 eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 NCBI_TaxID=3848;
 RN SEQUENCE FROM N.A.
 RC STRAIN=SH1; ;
 RA Xue Z.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 basic chain derived from a single precursor and linked by a
 disulfide bond (By similarity).
 CC -1- SIMILARITY: Belongs to the IIS seed storage protein (globulins)
 family.
 EMBL; X86970; CMA60533.1; -.
 DR PIR; S54802; S54802.
 DR HSSP; P04776; 1FXZ.
 DR GO; GO:0045735; P:nutrient reservoir activity; IEA.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR011051; RmLC.
 DR InterPro; IPR006044; Seedstore_11s.
 DR PROSITE; PRO0439; 11SG1G0BULIN.
 DR PROSITE; PS00305; IIS_SEED_STORAGE; 1.
 DR SEQUENCE 563 AA; 63797 MW; 4ACC765055AB9B1B CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 563;
 Best Local Similarity 100.0%; Pred. No. 0.78;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IPPGYPYWT 9
 Db 149 IPPGYPYWT 157

RESULT 7
 Q9SB11; PRELIMINARY; PRT; 563 AA.
 AC Q9SB11;
 DR 01-MAY-2000 (TRIMBULrel. 13, Created)
 DR 01-MAY-2000 (TRIMBULrel. 13, Last sequence update)
 DR 01-OCT-2003 (TRIMBULrel. 25, Last annotation update)
 DE Glycinin.
 OS Glycine max (Soybean).
 RA Chen S.; Araihira M.; Fukazawa C.;
 RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 basic chain derived from a single precursor and linked by a
 disulfide bond (By similarity).
 CC -1- SIMILARITY: Belongs to the IIS seed storage protein (globulins)
 CC family.
 DR EMBL; AB040462; BAA74953.1; -.
 DR PIR; PQ0199; PQ0199.
 DR HSSP; P04776; 1FXZ.
 DR GO; GO:0045735; P:nutrient reservoir activity; IEA.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR011051; RmLC.
 DR InterPro; IPR006044; Seedstore_11s.
 DR Pfam; PF00190; Cupin; 2.
 DR PROSITE; PRO0439; 11SG1G0BULIN.
 DR PROSITE; PS00305; IIS_SEED_STORAGE; 1.
 DR SEQUENCE 563 AA; 63797 MW; 4ACC765055AB9B1B CRC64;
 Query Match 100.0%; Score 58; DB 2; Length 563;
 Best Local Similarity 100.0%; Pred. No. 0.78;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IPPGYPYWT 9
 Db 149 IPPGYPYWT 157

RESULT 8
 Q43672; PRELIMINARY; PRT; 136 AA.
 AC Q43672;
 DT 01-NOV-1996 (TRIMBULrel. 01, Created)
 DT 01-JUN-2003 (TRIMBULrel. 24, Last annotation update)
 DE Legumin; legumin-related high molecular weight polypeptide
 DE (Fragment).
 GN Name=Le1B161;
 OS Vicia faba (Broad bean).
 OC Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Cupin; Eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 NCBI_TaxID=3906;

[1] SEQUENCE FROM N.A.
RC TISSUE=Cotyledons;
RX MEDLINE=94272010; PubMed=803694;
RA Heim U., Baumlein H., Wobus U.;
RT "The legumin gene family: reconstructed Vicia faba legumin gene
encoding a high-molecular-weight subunit is related to type B genes."
RP Plant Mol. Biol. 25:131-135 (1994).
DR EMBL; 226487; CABAB1261.1; -.
DR HSSP; P04776; 1PXXZ.
DR InterPro: IPR00645; Cupin_region.
DR InterPro: IPR007113; Cupin_region.
DR InterPro: IPR011051; RmIC_like_cupin.
DR InterPro: IPR01190; Cupin_1.
DT NON_TER 1 136 136 AA; 15317 MW; 3C24820F2630F069 CRC64;
SEQUENCE 136 AA; 15317 MW; 3C24820F2630F069 CRC64;
Query Match 98.3%; Score 57; DB 2; Length 564;
Best Local Similarity 88.9%; Pred. No. 0.26; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0; Index 0; Gaps 0;

Qy 1 IPPGYPYNT 9
Db 142 IPPGYPYNT 150

RESULT 10
O24294 PRELIMINARY; PRT; 566 AA.
ID O24294; PRELIMINARY;
AC 024294; 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Legumin (Minor small) precursor.
Name=legS;
PDB PDB: 1LEG
RN Pium sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
NCBI_TaxID=3888;
[1] RN SEQUENCE FROM N.A.
RP TISSUE=Cotyledon;
RA Bown D.O., Gatehouse J.A.;
RA Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN [2] RN
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RA Bown D.P.;
RL Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
basic chain derived from a single precursor and linked by a
disulfide bond (By similarity).
CC -1- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
CC family.
DR EMBL; X67124; CAA47109.1; -.
DR PIR; T06453; T06453.
DR HSSP; P04776; 1PXXZ.
DR GO; GO:004735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR006045; Cupin.
DR InterPro; IPR007113; Cupin_region.
DR InterPro; IPR011051; RmIC_like_cupin.
DR InterPro; IPR006044; Seedstore_11s.
DR PRINTS; PR00439; 11S_GLOBULIN.
DR PROSITE; PS00305; 11S_SEED_STORAGE; 1.
DR PROSITE; PS00697; DNA_LIGASE_ALI; UNKNOWN_1.
DR PROSITE; PS00697; DNA_LIGASE_ALI; UNKNOWN_1.
KW seed storage protein; Signal; storage protein.
FT SIGNAL 56 AA; 64872 MW; 663A80D2E265359CE CRC64;
SEQUENCE 56 AA;
Query Match 98.3%; Score 57; DB 2; Length 566;
Best Local Similarity 88.9%; Pred. No. 1.1; Mismatches 0; Index 0; Gaps 0;

Qy 1 IPPGYPYNT 9
Db 144 IPPGYPYNT 152

RESULT 11
O9FBC5 PRELIMINARY; PRT; 536 AA.
ID O9FBC5; 01-MAR-2001 (TREMBLrel. 16, Created)
AC 09FBC5; 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE G1ycinin subunit G7.

SEQUENCE 564 AA; 64502 MW; 568E497245A1915A CRC64;

GN Name=Gy7;
 OS Glycine max (Soybean).
 OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; rosids;
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TAXID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Beilinson V., Chen Z., Shoemaker R.C., Fischer R.L., Goldberg R.B.,
 Nielsen N.C.;
 RA "Genomic organization of Glycinin genes in soybean.";
 RT Theor. Appl. Genet. 104:1132-1140 (2002).
 DR EMBL; AF319777; AUG42489.1;
 DR HSSP; P04776; 1FYZ;
 DR GO; GO:0045735; F-nutrient reservoir activity; IEA.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR007113; Cupin region.
 DR InterPro; IPR011051; RmIC-like_cupin.
 DR Pfam; PF00190; Cupin; 2.
 DR PRINTS; PR00139; 11SGLOBULIN.
 SQ SEQUENCE 536 AA; 60486 MW; 40F452FAA067FBC7 CRC64;
 Best Local Similarity 96.6%; Score 56; DB 2; Length 536;
 Matches 7; Conservative 2; N mismatches 0; Indels 0; Gaps 0;
 Qy 1 IPPGVPyNT 9
 Db 137 VPPGIPYWT 145

RESULT 12

Q6DR94 ID Q6DR94 PRELIMINARY; PRT; 536 AA.
 AC Q6DR94; (TREMBUREL. 28, Created)
 DT 01-OCT-2004 (TREMBUREL. 28, Last sequence update)
 DT 01-OCT-2004 (TREMBUREL. 28, Last annotation update)
 DE Glycinin subunit G7.
 OS Glycine max (Soybean).
 OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; rosids;
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TAXID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Mi D., Li J.Y., Zhang W.,
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY649099; AAT68239.1; -.
 SQ SEQUENCE 536 AA; 60514 MW; 94BP37198D1C4468 CRC64;

Query Match 96.6%; Score 56; DB 2; Length 536;
 Best Local Similarity 97.8%; Score 56; DB 2; Length 536;
 Matches 7; Conservative 2; N mismatches 0; Indels 0; Gaps 0;

Qy 1 IPPGVPyNT 9
 Db 137 VPPGIPYWT 145

RESULT 13

ID GLC4_SOYBN STANDARD; PRT; 562 AA.
 AC P02858; (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 05, Last sequence update)
 DT 13-AUG-1987 (Rel. 44, Last annotation update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4
 DE subunit; Glycinin B3 subunit].
 Name=GY4;

OS Glycine max (Soybean).
 OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; rosids;
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TAXID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=cv. Bonminiori;
 MEDLINE=85210642; PubMed=2988947;
 RX RA Momma T., Negoro T., Hirano H., Matsumoto A., Ueda K., Fukazawa C.;
 RT "Glycinin A5A4B3 mRNA: cDNA cloning and nucleotide sequencing of a
 RT splitting storage protein subunit of soybean.";
 RL Eur. J. Biochem. 149:491-496 (1985).
 RN [2]
 RP SEQUENCE (A4/A5 SUBUNITS).
 RC STRAIN=cv. Bonminiori
 RA Hirano H., Fukazawa C., Harada K.;
 RT "The primary structures of the A4 and A5 subunits are highly
 RT homologous to that of the A3 subunit in the Glycinin seed storage
 protein of soybean.";
 RL FEBS Lett. 181:124-128 (1985).
 RN [3]
 RP SEQUENCE OF 181-386 FROM N.A.
 RC STRAIN=cv. CX635-1-1-1;
 RA Scallion B.J., Dickinson C.D., Nielsen N.C.;
 RT "Characterization of a null-allele for the Gy4 glycinin gene from
 soybean.";
 RL Mol. Gen. Genet. 208:107-113 (1987).
 CC -|- FUNCTION: Glycinin is the major seed storage protein of soybean.
 CC -|- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 CC basic chain derived from a single precursor and linked by a
 CC disulfide bond.
 CC -|- SIMILARITY: Belongs to the IIS seed storage protein (globulins)
 CC family.
 CC ---
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 CC ---
 CC DR EMBL; X02626; CAA26478.1; -.
 CC DR EMBL; X05652; CAB7802.1; -.
 CC DR PIR; A91145; FWSYGS.
 CC DR HSSEB; P04776; 1PKZ.
 CC DR InterPro; IPR006045; Cupin.
 CC DR InterPro; IPR011051; RmIC-like_cupin.
 CC DR InterPro; IPR016044; Seedstore_11s.
 CC DR Pfam; PF00190; Cupin; 2.
 CC DR PRINTS; PR00339; 11SGJUBLIN.
 CC DR PROSITE; PS00305; I15_SEED_STORAGE; 1.
 CC DR Direct protein sequencing; Multigene family; Seed storage protein;
 CC KW Signal.
 CC FT SIGNAL; 1
 CC FT ; CHAIN 1
 CC FT CHAIN 24
 CC FT CHAIN 121
 CC FT CHAIN 378
 CC FT DISULFID 562
 CC FT DISULFID 108
 CC FT CONFLICT 384
 CC FT CONFLICT 29
 CC FT CONFLICT 92
 CC FT CONFLICT 29
 CC FT CONFLICT 82
 CC FT CONFLICT 86
 CC FT CONFLICT 94
 CC FT CONFLICT 103
 CC FT CONFLICT 101
 CC FT CONFLICT 105
 CC FT CONFLICT 117
 CC FT CONFLICT 253
 CC FT CONFLICT 335
 CC SEQUENCE 562 AA; 63387 MW; FSA06B0856B9BB0D6 CRC64;
 SQ Query Match 89.7%; Score 52; DB 1; Length 562;
 Best Local Similarity 88.9%; Pred. No. 7;

